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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,760

DATE: 05/31/2002

TIME: 08:32:21

Input Set : A:\U609011.app

Output Set: N:\CRF3\05312002\J006760.raw

p6

3 <110> APPLICANT: Koide, Shohei
 5 <120> TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND
 6 TO TARGET PROTEINS AND USE THEREOF
 8 <130> FILE REFERENCE: 176/60901
 10 <140> CURRENT APPLICATION NUMBER: 10/006,760
 11 <141> CURRENT FILING DATE: 2001-11-19
 13 <150> PRIOR APPLICATION NUMBER: 60/249,756
 14 <151> PRIOR FILING DATE: 2000-11-17
 16 <160> NUMBER OF SEQ ID NOS: 73
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 308
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <400> SEQUENCE: 1
 26 catatgcagg tttctgatgt tccgcgtgac ctggaagttg ttgctgacgac cccgactagc 60
 27 ctgctgatca gctgggatgc tctgcagtt accgtgcgtt attaccgtat cacgtacggt 120
 28 gaaaccggtg gtaactcccc gggtcaggaa ttcactgtac ctggttccaa gtctactgct 180
 29 accatcagcg gcctgaaacc gggtgtcgac tataccatca ctgtatacgc tgttactggc 240
 30 cgtgggtgaca gcccagcgag ctccaagcca atctcgatta actaccgtac ctagtaactc 300
 31 gaggatcc 308
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 96
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Homo sapiens
 39 <400> SEQUENCE: 2
 40 Met Gln Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
 41 1 5 10 15
 43 Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg
 44 20 25 30
 46 Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
 47 35 40 45
 49 Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu
 50 50 55 60
 52 Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg
 53 65 70 75 80
 55 Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr
 56 85 90 95
 62 <210> SEQ ID NO: 3
 63 <211> LENGTH: 96
 64 <212> TYPE: PRT
 65 <213> ORGANISM: Artificial Sequence
 67 <220> FEATURE:

ENTERED

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68 <223> OTHER INFORMATION: Description of Artificial Sequence: mutant tenth
 69 fibronectin type 3 domain of human fibronectin

71 <220> FEATURE:

72 <221> NAME/KEY: UNSURE

73 <222> LOCATION: (9)

74 <223> OTHER INFORMATION: X at position 9 is either Asn or Lys

76 <400> SEQUENCE: 3

77 Met Gln Val Ser Asp Val Pro Arg Xaa Leu Glu Val Val Ala Ala Thr

78 1 5 10 15

80 Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg

81 20 25 30

83 Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln

84 35 40 45

86 Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu

87 50 55 60

89 Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg

90 65 70 75 80

92 Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr

93 85 90 95

99 <210> SEQ ID NO: 4

100 <211> LENGTH: 618

101 <212> TYPE: DNA

102 <213> ORGANISM: Artificial Sequence

104 <220> FEATURE:

105 <223> OTHER INFORMATION: Description of Artificial Sequence: B42-FNfn10

106 fusion protein coding region

108 <220> FEATURE:

109 <221> NAME/KEY: unsure

110 <222> LOCATION: (112)..(113)

111 <223> OTHER INFORMATION: N at positions 112 and 113 can be A, C, T, or G

113 <220> FEATURE:

114 <221> NAME/KEY: unsure

115 <222> LOCATION: (115)..(116)

116 <223> OTHER INFORMATION: N at positions 115 and 116 can be A, C, T, or G

118 <220> FEATURE:

119 <221> NAME/KEY: unsure

120 <222> LOCATION: (118)..(119)

121 <223> OTHER INFORMATION: N at positions 118 and 119 can be A, C, T, or G

123 <220> FEATURE:

124 <221> NAME/KEY: unsure

125 <222> LOCATION: (121)..(122)

126 <223> OTHER INFORMATION: N at positions 121 and 122 can be A, C, T, or G

128 <220> FEATURE:

129 <221> NAME/KEY: unsure

130 <222> LOCATION: (124)..(125)

131 <223> OTHER INFORMATION: N at positions 124 and 125 can be A, C, T, or G

133 <220> FEATURE:

134 <221> NAME/KEY: unsure

135 <222> LOCATION: (268)..(269)

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Input Set : A:\U609011.app

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136 <223> OTHER INFORMATION: N at positions 268 and 269 can be A, C, T, or G
138 <220> FEATURE:
139 <221> NAME/KEY: unsure
140 <222> LOCATION: (271)..(272)
141 <223> OTHER INFORMATION: N at positions 271 and 272 can be A, C, T, or G
143 <220> FEATURE:
144 <221> NAME/KEY: unsure
145 <222> LOCATION: (274)..(275) /
146 <223> OTHER INFORMATION: N at positions 274 and 275 can be A, C, T, or G
148 <220> FEATURE:
149 <221> NAME/KEY: unsure
150 <222> LOCATION: (277)..(278) /
151 <223> OTHER INFORMATION: N at positions 277 and 278 can be A, C, T, or G
153 <220> FEATURE:
154 <221> NAME/KEY: unsure
155 <222> LOCATION: (280)..(281) /
156 <223> OTHER INFORMATION: N at positions 280 and 281 can be A, C, T, or G
158 <220> FEATURE:
159 <221> NAME/KEY: unsure /
160 <222> LOCATION: (283)..(284)
161 <223> OTHER INFORMATION: N at positions 283 and 284 can be A, C, T, or G
163 <220> FEATURE:
164 <221> NAME/KEY: unsure
165 <222> LOCATION: (286)..(287)
166 <223> OTHER INFORMATION: N at positions 286 and 287 can be A, C, T, or G
168 <220> FEATURE:
169 <221> NAME/KEY: unsure
170 <222> LOCATION: (114)
171 <223> OTHER INFORMATION: K at position 114 can be G or T
173 <220> FEATURE:
174 <221> NAME/KEY: unsure /
175 <222> LOCATION: (117)
176 <223> OTHER INFORMATION: K at position 117 can be G or T
178 <220> FEATURE:
179 <221> NAME/KEY: unsure
180 <222> LOCATION: (120)
181 <223> OTHER INFORMATION: K at position 120 can be G or T
183 <220> FEATURE:
184 <221> NAME/KEY: unsure
185 <222> LOCATION: (123) /
186 <223> OTHER INFORMATION: K at position 123 can be G or T
188 <220> FEATURE:
189 <221> NAME/KEY: unsure /
190 <222> LOCATION: (126)
191 <223> OTHER INFORMATION: K at position 126 can be G or T
193 <220> FEATURE:
194 <221> NAME/KEY: unsure
195 <222> LOCATION: (270) /
196 <223> OTHER INFORMATION: K at position 270 can be G or T

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198 <220> FEATURE:
199 <221> NAME/KEY: unsure
200 <222> LOCATION: (273)
201 <223> OTHER INFORMATION: K at position 273 can be G or T
203 <220> FEATURE:
204 <221> NAME/KEY: unsure
205 <222> LOCATION: (276)
206 <223> OTHER INFORMATION: K at position 276 can be G or T
208 <220> FEATURE:
209 <221> NAME/KEY: unsure
210 <222> LOCATION: (279)
211 <223> OTHER INFORMATION: K at position 279 can be G or T
213 <220> FEATURE:
214 <221> NAME/KEY: unsure
215 <222> LOCATION: (282)
216 <223> OTHER INFORMATION: K at position 282 can be G or T
218 <220> FEATURE:
219 <221> NAME/KEY: unsure
220 <222> LOCATION: (285)
221 <223> OTHER INFORMATION: K at position 285 can be G or T
223 <220> FEATURE:
224 <221> NAME/KEY: unsure
225 <222> LOCATION: (288)
226 <223> OTHER INFORMATION: K at position 288 can be G or T
228 <400> SEQUENCE: 4
229 atggactaca aggacgacga tgacaagggt atgcagggtt ctgatgttcc gaccgacctg 60
W--> 230 gaagttgttg ctgcgacccc gactagcctg ctgatcagct gggatgctcc tnnknnknnk' 120
W--> 231 nnknnktatt accgtatcac gtacgggtgaa accgggtgga actccccggt tcaggaattc 180
W--> 232 actgtacctg gttccaagtc tactgctacc atcagcggcc tgaaaccggg tgcgactat 240
233 accatcactg tatacgtgtt tactggcnnk nnknnknnkn nknnknnktc caagccaatc 300
234 tcgattaact accgtaccag tggtagcggg ggttcccctc caaaaaagaa gagaaaggta 360
235 gctggatatca ataaagatat cgaggagtgc aatgccatca ttgagcagtt tatcgactac 420
236 ctgcgcaccg gacaggagat gccgatggaa atggcggatc aggcgattaa cgtgggtgccg 480
237 ggcattgacgc cgaaaacat tcttcacgcc gggccgccga tccagcctga ctggctgaaa 540
238 tcgaatgggtt ttcattgaaat tgaagcggat gttaacgata ccagcctctt gctgagtgga 600
239 gattaactcg aggcattgc 618
242 <210> SEQ ID NO: 5
243 <211> LENGTH: 201
244 <212> TYPE: PRT
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial
249 B42-FNfn10 fusion protein
251 <220> FEATURE:
252 <221> NAME/KEY: UNSURE
253 <222> LOCATION: (38)..(42)
254 <223> OTHER INFORMATION: Xaa at any position can be any amino acid
256 <220> FEATURE:
257 <221> NAME/KEY: UNSURE

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Input Set : A:\U609011.app

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258 <222> LOCATION: (90)..(96)

259 <223> OTHER INFORMATION: Xaa at any position can be any amino acid

261 <400> SEQUENCE: 5

262 Met Asp Tyr Lys Asp Asp Asp Asp Lys Gly Met Gln Val Ser Asp Val
 263 1 5 10 15

265 Pro Thr Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile
 266 20 25 30

268 Ser Trp Asp Ala Pro Xaa Xaa Xaa Xaa Xaa Tyr Tyr Arg Ile Thr Tyr
 269 35 40 45

271 Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly
 272 50 55 60

274 Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr
 275 65 70 75 80

277 Thr Ile Thr Val Tyr Ala Val Thr Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 278 85 90 95

280 Ser Lys Pro Ile Ser Ile Asn Tyr Arg Thr Ser Gly Thr Gly Gly Ser
 281 100 105 110

283 Pro Pro Lys Lys Lys Arg Lys Val Ala Gly Ile Asn Lys Asp Ile Glu
 284 115 120 125

286 Glu Cys Asn Ala Ile Ile Glu Gln Phe Ile Asp Tyr Leu Arg Thr Gly
 287 130 135 140

289 Gln Glu Met Pro Met Glu Met Ala Asp Gln Ala Ile Asn Val Val Pro
 290 145 150 155 160

292 Gly Met Thr Pro Lys Thr Ile Leu His Ala Gly Pro Pro Ile Gln Pro
 293 165 170 175

295 Asp Trp Leu Lys Ser Asn Gly Phe His Glu Ile Glu Ala Asp Val Asn
 296 180 185 190

298 Asp Thr Ser Leu Leu Leu Ser Gly Asp
 299 195 200

302 <210> SEQ ID NO: 6

303 <211> LENGTH: 96

304 <212> TYPE: PRT

305 <213> ORGANISM: Artificial Sequence

307 <220> FEATURE:

308 <223> OTHER INFORMATION: Description of Artificial Sequence: FNfn10
 309 polypeptide monobody

311 <220> FEATURE:

312 <221> NAME/KEY: UNSURE

313 <222> LOCATION: (28)..(32)

314 <223> OTHER INFORMATION: Xaa at any position can be any amino acid

316 <220> FEATURE:

317 <221> NAME/KEY: UNSURE

318 <222> LOCATION: (80)..(86)

319 <223> OTHER INFORMATION: Xaa at any position can be any amino acid

321 <400> SEQUENCE: 6

322 Met Gln Val Ser Asp Val Pro Thr Asp Leu Glu Val Val Ala Ala Thr
 323 1 5 10 15

325 Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Xaa Xaa Xaa Xaa Xaa
 326 20 25 30

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\U609011.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 9
Seq#:4; N Pos. 112,113,115,116,118,119,121,122,124,125,268,269,271,272,274
Seq#:4; N Pos. 275,277,278,280,281,283,284,286,287
Seq#:5; Xaa Pos. 38,39,40,41,42,90,91,92,93,94,95,96
Seq#:6; Xaa Pos. 28,29,30,31,32,80,81,82,83,84,85,86
Seq#:7; N Pos. 409,410,412,413,415,416,418,419,421,422,424,425,427,428
Seq#:8; Xaa Pos. 137,138,139,140,141,142,143
Seq#:9; Xaa Pos. 18,19,20,21,22,23,24
Seq#:10; N Pos. 439,440,442,443,445,446,448,449,451,452,595,596,598,599,601
Seq#:10; N Pos. 602,604,605,607,608,610,611,613,614
Seq#:11; Xaa Pos. 147,148,149,150,151,199,200,201,202,203,204,205
Seq#:12; Xaa Pos. 28,29,30,31,32,80,81,82,83,84,85,86
Seq#:13; N Pos. 595,596,598,599,601,602,604,605,607,608,610,611,613,614,616
Seq#:13; N Pos. 617,619,620,622,623,625,626,628,629,631,632,634,635,637,638
Seq#:13; N Pos. 640,641
Seq#:14; Xaa Pos. 199,200,201,202,203,204,205,206,207,208,209,210,211,212
Seq#:14; Xaa Pos. 213,214
Seq#:15; Xaa Pos. 80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95
Seq#:20; Xaa Pos. 2,3
Seq#:32; Xaa Pos. 2,3